

EXHIBIT D



56321664

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Integrated BRACAnalysis® with MyRisk™ Hereditary Cancer Test

MyRisk Genetic Result

MyRisk™
Hereditary Cancer Test

RECEIVING HEALTHCARE PROVIDER

Frederick Dold, MD
Alliance Cancer Specialists
1311 BRISTOL PIKE STE 100
BENSALEM, PA 19020

SPECIMEN

Specimen Type: Blood
Draw Date: Jan 14, 2025
Accession Date: Jan 15, 2025
Report Date: Jan 29, 2025

PATIENT

Legal Name: Voelker, Kevin
Date of Birth: [REDACTED]
Patient ID:
Sex at Birth: M
Accession #: 05258003-BLD
Requisition #: 11770109

GENETIC RESULT: POSITIVE - CLINICALLY SIGNIFICANT MUTATION IDENTIFIED
**CLINICAL HISTORY ANALYSIS: NO ADDITIONAL MANAGEMENT GUIDELINES IDENTIFIED
BASED ON THE CLINICAL HISTORY PROVIDED**

Other clinical factors may influence individualized management. This analysis may be incomplete if details about cancer diagnoses, ages, family relationships or other factors were omitted or ambiguous. If this patient also has a clinically significant mutation, the recommendations based on the clinical history analysis should be considered in light of the possibility that this mutation explains all or some of the cancer history in the family.

GENE	MUTATION	INTERPRETATION
CHEK2	c.1100del (p.Thr367Metfs*15) Heterozygous	High Risk This patient has CHEK2-associated cancer risk.

DETAILS ABOUT: CHEK2 c.1100del (p.Thr367Metfs*15): NM_007194.3
Functional Significance: Deleterious - Abnormal Protein Production and/or Function

The heterozygous germline CHEK2 mutation c.1100del is predicted to result in the premature truncation of the CHEK2 protein at amino acid position 381 (p.Thr367Metfs*15).

Clinical Significance: High Risk

This mutation is associated with increased cancer risk and should be regarded as clinically significant.

ADDITIONAL FINDINGS: NO VARIANT(S) OF UNCERTAIN SIGNIFICANCE (VUS) IDENTIFIED

Details About Non-Clinically Significant Variants: All individuals carry DNA changes (i.e., variants), and most variants do not increase an individual's risk of cancer or other diseases. When identified, variants of uncertain significance (VUS) are reported. Likely benign variants (Favor Polymorphisms) and benign variants (Polymorphisms) are not reported and available data indicate that these variants most likely do not cause increased cancer risk. Present evidence does not suggest that non-clinically significant variant findings be used to modify patient medical management beyond what is indicated by the personal and family history and any other clinically significant findings.

Variant Classification: Myriad's myVision™ Variant Classification Program performs ongoing evaluations of variant classifications. In certain cases, healthcare providers may be contacted for more clinical information or to arrange family testing to aid in variant classification. When new evidence about a variant is identified and determined to result in clinical significance and management change, that information will automatically be made available to the healthcare provider through an amended report.

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 MyRisk Genetic Result
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MyRisk Genetic Result

Name: Voelker, Kevin

DOB: A [REDACTED]

Accession #: 05258003-BLD

Report Date: Jan 29, 2025

ADDITIONAL INFORMATION

Genes Analyzed: Sequencing (seq) and large rearrangement analyses were performed for all coding exons in the following genes, unless otherwise indicated:

APC, ATM, AXIN2, BAP1, BARD1, BMPR1A, BRCA1, BRCA2, BRIP1, CDH1, CDK4, CDKN2A, CHEK2, CTNNA1, FH, FLCN, HOXB13 (seq only), MEN1, MET, MLH1, MSH2, MSH3 (excluding repetitive portions of exon 1), MSH6, MUTYH, NTHL1, PALB2, PMS2, PTEN, RAD51C, RAD51D, SDHA, SDHB, SDHC, SDHD, SMAD4, STK11, TP53, TSC1, TSC2, VHL.

Limited promoter regions may also be analyzed for large rearrangements.

Sequencing (seq) and/or large rearrangement (LR) analyses were performed only for the gene portions indicated in parenthesis for the following genes:

EGFR (exons 18-21, seq and LR), EPCAM (exons 8-9, LR only), GREM1 (exon 1 and upstream regulatory regions, LR only), MITF (c.952, seq only), POLE (exonuclease domain, seq only), POLD1 (exonuclease domain, seq only), RET (exons 5, 8, 10, 11, 13-16 seq and LR), TERT (promoter region 71 bases upstream of the translation start, c.-71_-1, seq only).

** Other genes not analyzed with this test may also be associated with cancer.

Indication for Testing: It is our understanding that this individual was identified for testing due to a personal or family history suggestive of a hereditary predisposition for cancer.

Patient Information: Sex assigned at birth is a label given to an individual at birth, typically "male" or "female". In this report, the terms "male", "female", "he", "she", "woman", and "man" refer to sex assigned at birth.

Associated Cancer Risks and Clinical Management: The "MyRisk Management Tool" associated with this report provides a summary of cancer risk and professional society medical management guidelines that may be useful in developing a plan for this patient based on any clinically significant test results and/or reported personal/family history. In some cases, a MyRisk Management Tool cannot be provided, such as when the result has a special interpretation or includes a mutation with unusual characteristics.

Analysis Description: The Technical Specifications summary (myriad.com/technical-specifications) describes the analysis, method, performance, nomenclature, and interpretive criteria of this test. Current testing technologies are unable to definitively determine whether a variant is germline or somatic in origin, which may significantly impact risk estimates and medical management; therefore, these results should be correlated with this patient's personal and family history. The interpretation of this test may also be impacted if the patient has a hematologic malignancy or an allogeneic bone marrow transplant.

CLASSIFICATION DISCLAIMER

THE CLASSIFICATION AND INTERPRETATION OF ALL VARIANTS IDENTIFIED IN THIS ASSAY REFLECTS THE CURRENT STATE OF MYRIAD'S SCIENTIFIC UNDERSTANDING AT THE TIME THIS REPORT WAS ISSUED. VARIANT CLASSIFICATION AND INTERPRETATION MAY CHANGE FOR A VARIETY OF REASONS, INCLUDING BUT NOT LIMITED TO, IMPROVEMENTS TO CLASSIFICATION TECHNIQUES, AVAILABILITY OF ADDITIONAL SCIENTIFIC INFORMATION, AND OBSERVATION OF A VARIANT IN MORE PATIENTS.

Please contact Myriad Medical Services at 1-800-469-7423 X 3850 to discuss any questions regarding this result.

These test results should only be used in conjunction with the patient's clinical history and any previous analysis of appropriate family members. The patient's clinical history and test results should not be disclosed to a third party, unless related to treatment or payment for treatment, without the patient's express written authorization. It is strongly recommended that these results be communicated to the patient in a setting that includes appropriate genetic consultation. This test was developed and its performance characteristics determined by Myriad Genetic Laboratories. It has not been cleared or approved by the U.S. Food and Drug Administration (FDA). The FDA has determined that clearance or approval for laboratory-developed tests is not required.

This Authorized Signature
pertains to this laboratory report:

Benjamin B. Roa, PhD
Diplomate ABMGG
Laboratory Director

Genetic testing was completed by CLIA and CAP accredited laboratories in the United States located at: 320 Wakara Way, Salt Lake City, UT 84108 and 322 N 2200 W, Salt Lake City, UT 84116 CLIA IDs: 46D0880690, 46D2275645
The following personnel codes and laboratory director signature may reflect remote review of digital data: 572, 3028

Patricia Nis

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MyRisk Genetic Result
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Integrated BRACAnalysis® with MyRisk™ Hereditary Cancer Test
Clinical & Cancer Family History Information

MyRisk™
 Hereditary Cancer Test

RECEIVING HEALTHCARE PROVIDER	SPECIMEN	PATIENT
Frederick Dold, MD Alliance Cancer Specialists 1311 BRISTOL PIKE STE 100 BENSalem, PA 19020	Specimen Type: Blood Draw Date: Jan 14, 2025 Accession Date: Jan 15, 2025 Report Date: Jan 29, 2025	Legal Name: Voelker, Kevin Date of Birth: [REDACTED] Patient ID: [REDACTED] Sex at Birth: M Accession #: 05258003-BLD Requisition #: 11770109

PERSONAL / FAMILY CANCER HISTORY SUMMARY		
FAMILY MEMBER	CANCER / CLINICAL DIAGNOSIS	AGE AT DIAGNOSIS
Patient	Kidney/Renal	63
Family History	None	

The clinical information displayed here was provided by a qualified healthcare provider on the Test Request Form and other documents, and was not verified by Myriad. Female relatives refers to sex assigned at birth, which is a label given to an individual at birth, typically "male" or "female". Family members listed as "other" are not included in a Tyrer-Cuzick breast cancer risk estimate or other personal/family history assessments. For more information see the Specifications for Personal/Family History Analysis at <http://myriad.com/technical-specifications>.

The accuracy and completeness of the information provided in the Clinical and Cancer Family History Information section of the report (e.g. height and weight, age of menarche) may significantly affect the accuracy of breast cancer risk estimates provided based on either Tyrer-Cuzick or RiskScore. The impact of breast surgeries and hormone therapy (except hormone replacement therapy) have not been assessed or validated for Tyrer-Cuzick and RiskScore.

RiskScore is not valid, and may significantly over- or under-estimate breast cancer risk for individuals who do not meet the eligibility criteria in effect when the testing was performed. The current criteria are: 1) sex assigned at birth is female 2) age is 18 to 84 years, 3) no personal history of breast cancer, LCIS, hyperplasia (with or without atypia), or a breast biopsy with unknown results, 4) there is no mutation detected in a breast cancer risk gene (other than a monoallelic *CHEK2* mutation in a White/Non-Hispanic or Ashkenazi Jewish individual), 5) the individual's relatives have not been found to have a mutation in a high-penetrance breast cancer risk gene (*BRCA1*, *BRCA2*, *CDH1*, *PALB2*, *PTEN*, *STK11*, *TP53*, a biallelic mutation in *CHEK2*, or the specific mutation c.7271T>G (p.Val2424Gly) in *ATM*) and 6) the sample was submitted with a current Test Request Form and the ordering healthcare provider has not determined that RiskScore is inappropriate for the patient. If this is an amended report for a patient tested in the past, please refer to the MyRisk Technical Specifications at <http://myriad.com/technical-specifications> for the eligibility criteria in effect at the time of the original testing.

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Clinical Information
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Accession #: 05258003-BLD
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GENETIC RESULT: POSITIVE - CLINICALLY SIGNIFICANT MUTATION IDENTIFIED



CLINICAL HISTORY ANALYSIS: NO ADDITIONAL MANAGEMENT GUIDELINES IDENTIFIED BASED ON THE CLINICAL HISTORY PROVIDED

Other clinical factors may influence individualized management. This analysis may be incomplete if details about cancer diagnoses, ages, family relationships or other factors were omitted or ambiguous. If this patient also has a clinically significant mutation, the recommendations based on the clinical history analysis should be considered in light of the possibility that this mutation explains all or some of the cancer history in the family.

GENE

MUTATION

THIS GENETIC TEST RESULT IS ASSOCIATED WITH THE FOLLOWING CANCER RISKS:

CHEK2

c.1100del (p.Thr367Metfs*15)
Heterozygous

ELEVATED RISK: Male Breast, Colorectal

Please see the Genetic Test Result for more details on any variant(s) detected in this patient, including variant classification information.

The terms "male", "female", "he", "she", "women", and "men" refer to sex assigned at birth.

ADDITIONAL FINDINGS: NO VARIANT(S) OF UNCERTAIN SIGNIFICANCE (VUS) IDENTIFIED

CLINICAL OVERVIEW OF GENETIC FINDINGS

CHEK2-associated cancer risk

- This patient has been found to have a mutation in the *CHEK2* gene. Most women with *CHEK2* mutations have a risk for breast cancer that is significantly increased over the 12.5% lifetime risk for women in the general population of the United States. Men with *CHEK2* mutations also have an increased risk for breast cancer.
- Estimates of cancer risk for men and women with *CHEK2* mutations vary widely and are strongly influenced by family history. In cases where there is no family history of one of these cancers, the risk for a patient with a *CHEK2* mutation may be lower than in cases where that cancer has been diagnosed in one or more close relatives. Therefore, the family history of a patient should be considered when deciding on the most appropriate strategies to manage cancer risk, with more aggressive strategies targeted to patients with significant family histories of related cancers.
- Individuals with *CHEK2* mutations may have an elevated risk for colorectal cancer, and the National Comprehensive Cancer Network (NCCN) has provided screening recommendations to address this possible risk.
- Some studies have described a possible increased risk for a wide range of cancers in patients with *CHEK2* mutations, including prostate, gastric, thyroid, renal, hematological malignancies, testicular germ cell tumors, and other malignancies. However, these studies are not conclusive and there are currently no medical management guidelines to address these possible risks.

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MyRisk Management Tool
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MyRisk Management Tool

Name: Voelker, Kevin

DOB: [REDACTED]

Accession #: 05258003-BLD

Report Date: Jan 29, 2025

- Although there are increased risks for cancer in men and women with mutations in *CHEK2*, there are interventions that may reduce these risks. Guidelines from the National Comprehensive Cancer Network (NCCN) that may apply are listed below. Since information about the cancer risks associated with *CHEK2* mutations is relatively new, and there is still some uncertainty about the best ways to reduce these risks, it may be appropriate to interpret these results in consultation with cancer genetics experts in this emerging area of knowledge.

WHAT ARE THE PATIENT'S CANCER RISKS?

These risk tables show the clinically significant cancer risks identified as part of this patient's testing. Testing for some patients does not include some of the analyses listed:

- GENETIC RESULT: Mutations detected in any of the hereditary cancer genes included on the MyRisk panel.
- BREAST CANCER RISKS: RiskScore estimate of remaining lifetime breast cancer risk if 20% or greater
- CLINICAL HISTORY ANALYSIS for breast cancer risk: Tyrer-Cuzick model estimate of remaining lifetime breast cancer risk of 20% or greater
- CLINICAL HISTORY ANALYSIS for breast, colorectal, pancreatic, prostate and melanoma cancer: Analysis of the patient's personal and family history.

The risks for each of these results are provided separately. If the risk for any individual cancer is affected by more than one of these results, the risk associated with each finding is listed in a separate table. At this time, there is not enough information to estimate risks for cancers affected by more than one gene mutation, or risks based on both gene mutations and personal/family history.

Risks Due to *CHEK2*-associated cancer risk

CANCER TYPE	CANCER RISK	RISK FOR GENERAL POPULATION	RELATED TO
MALE BREAST			
To age 80	0.4%-1%	0.1%	<i>CHEK2</i>
COLORECTAL			
To age 80	Possibly elevated risk	2.8%	<i>CHEK2</i>

WHAT MANAGEMENT FOR CANCER RISKS SHOULD BE CONSIDERED?

This overview of clinical management guidelines is based on the patient's genetic test results and the Clinical History Analysis. Medical management guidelines are summarized from established medical societies, primarily the National Comprehensive Cancer Network (NCCN). If there are overlapping management guidelines for any individual cancer due to more than one of these results, the guidelines associated with each finding are listed in separate tables, even if they are the same. At this time, there are no medical society guidelines for how to adjust management when there are multiple sources of risk, such as from more than one gene mutation, or a mutation and a personal/family history of cancer. In these cases, it may be appropriate to use the most aggressive of the management options provided.

The overview provided below should not be used as the sole source of information to determine medical management. The references cited should always be consulted for more details and updates to the recommendations.

No information is provided related to treatment of a previous or existing cancer or polyps. The recommendation summaries below may require modification due to the patient's personal medical history, past surgeries and other treatments. Patients with a past history of cancer, benign tumors, or pre-cancerous findings may be candidates for long term surveillance and risk-reduction strategies beyond what is necessary for the treatment of their initial diagnosis. Any discussion of medical management options is for general information purposes only and does not constitute a recommendation. While genetic testing and medical society recommendations provide important and useful information, medical management decisions should be made in consultation between each patient and his or her healthcare provider.

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DOB: [REDACTED]

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Management Options for CHEK2-associated cancer risk

PROCEDURE	AGE TO BEGIN	FREQUENCY Unless otherwise indicated by findings	RELATED TO
MALE BREAST			
Currently there are no specific medical management guidelines for male breast cancer risk in mutation carriers. However, the increase in risk warrants consideration of options for male breast cancer screening, such as patient breast awareness education and clinical breast examinations. ^{1,2}	Individualized	NA	CHEK2
COLORECTAL			
Colonoscopy ³	40 years, or 10 years younger than the age of diagnosis for any first-degree relative with colorectal cancer	Every 5 years	CHEK2

FOR PATIENTS WITH A CANCER DIAGNOSIS

For patients with a gene mutation and a diagnosis of cancer, targeted therapies may be available as a treatment option for certain tumor types (e.g., PARP-inhibitors).⁴

NA

NA

CHEK2

1. Bevers TB, et al. NCCN Clinical Practice Guidelines in Oncology®: Breast Cancer Screening and Diagnosis. V 1.2022. Jun 2. Available at <https://www.nccn.org>.

2. Daly M, et al. NCCN Clinical Practice Guidelines in Oncology®: Genetic/Familial High-Risk Assessment: Breast, Ovarian and Pancreatic. V 3.2023. Feb 13. Available at <https://www.nccn.org>.

3. Gupta S, et al. NCCN Clinical Practice Guidelines in Oncology® Genetic/Familial High-Risk Assessment: Colorectal. V 1.2023. May 30. Available at <https://www.nccn.org>.

4. Schaeffer E, et al. NCCN Clinical Practice Guidelines in Oncology®: Prostate Cancer. V 1.2023. Sep 16. Available at <https://www.nccn.org>.

Notes for Personalized Management:

INFORMATION ON HOW CANCER RISKS AND MANAGEMENT ARE DETERMINED

The MyRisk Management Tool provides cancer risk levels based on analysis of genetic test results (see MyRisk Genetic Result) and a summary of medical society management recommendations based on both the genetic test results and a limited analysis of the patient's clinical history related to the risk for breast, colorectal, prostate, melanoma and pancreatic cancers. Here are some important points to understand as you interpret this test report and decide on the best plan for management:

- Comprehensive patient management. The management recommendations presented in this report are a summary of management options recommended by the National Comprehensive Cancer Network (NCCN) and other established medical societies and are general in nature. The patient's actual management should be modified based on personal medical history, surgeries and other treatments. A comprehensive risk assessment and management plan may take into account this report and other aspects of the patient's personal/family medical history (e.g., all known clinical diagnoses), as well as lifestyle, environmental and other factors.

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MyRisk Management Tool

Name: Vaelker, Kevin

DOB: Aug 11, 1961

Accession #: 05258003-BLD

Report Date: Jan 29, 2025

- Risk estimates based on provider-supplied information. Some of the risk estimates and management recommendation summaries provided in this report are based on our interpretation of information supplied by the ordering health care provider on the test request form (see Specifications for Personal/Family History analysis at myriad.com/technical-specifications). The patient's actual risks and appropriate management may be significantly different if details provided for cancer diagnoses, ages, family relationships or other factors were incorrect, omitted, ambiguous or have since changed. Please review the clinical history listed on the Clinical & Family History Information page of this report to make sure that the information used was provided and interpreted correctly.
- Variability in Tyer-Cuzick risk estimates. Tyer-Cuzick estimates of breast cancer risk can vary significantly based on the way in which the model is used, and the estimate provided here may be higher or lower than what would be calculated by other users. For complete details of how Myriad calculates Tyer-Cuzick risk estimates, including how Myriad handles information provided in a format not compatible with the model, please see the Specifications for Personal/Family History analysis at myriad.com/technical-specifications. These Specifications also include information for recalculating the Tyer-Cuzick breast cancer risk estimate if desired.
- What is meant by "High Risk" and "Elevated Risk"? In the Genetic Test Result Summary, a gene-associated cancer risk is described as "High Risk" for a cancer type if all of the following conditions are met: the absolute risk of cancer is approximately 5% or higher, the increase in risk over the general population is approximately 2 to 3-fold or higher, and there is significant data from multiple studies supporting the cancer risk estimate. A gene is described as "Elevated Risk" for a cancer type if there is sufficient data to support an increase in cancer risk over the general population risk, but not all criteria for "High Risk" are met.

INFORMATION FOR FAMILY MEMBERS

Family members should talk to their healthcare providers about hereditary cancer testing to help define their own risk and assist in the interpretation of this patient's genetic test result.

- This patient's relatives are at risk for carrying the same mutation(s) and associated cancer risks as this patient. Cancer risks for individuals who have this/these mutation(s) are provided below.
- Family members should talk to a healthcare provider about genetic testing. Close relatives such as parents, children, and siblings have the highest chance of having the same mutation(s) as this patient. Other more distant relatives such as cousins, parents' siblings, and grandparents also have a chance for carrying the same mutation(s). Testing of at-risk relatives can identify those family members with the same mutation(s) who may benefit from surveillance and early intervention. More resources for family testing are available at MySupport360.com.

Additional Information for *CHEK2*-associated cancer risk

- In rare instances, an individual may inherit mutations in both copies of the *CHEK2* gene, leading to significantly higher breast cancer risks than those in women with a single *CHEK2* mutation. The children of this patient are at risk of inheriting two *CHEK2* mutations only if the other parent is also a carrier of a *CHEK2* mutation. Screening the other biological parent of any children for *CHEK2* mutations may be appropriate. Alternatively, this patient's children may consider genetic testing for any mutations in the entire *CHEK2* gene.

CANCER RISK FOR *CHEK2* CLINICALLY SIGNIFICANT MUTATION

CANCER TYPE	CANCER RISK	RISK FOR GENERAL POPULATION
FEMALES		
FEMALE BREAST		
To age 80	20%-31%	10.7%
Second primary within 10 years of first breast cancer diagnosis	7%-29%	3.5%
MALES		
MALE BREAST		
To age 80	0.4%-1%	0.1%



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DOB: [REDACTED]

Accession #: 05258003-BLD

Report Date: Jan 29, 2025

CANCER RISK FOR CHEK2 CLINICALLY SIGNIFICANT MUTATION

CANCER TYPE	CANCER RISK	RISK FOR GENERAL POPULATION
		FEMALES AND MALES
COLORECTAL	To age 80	Possibly elevated risk 2.8%

Please contact Myriad Medical Services at 1-800-469-7423 X 3850 to discuss any questions regarding this result.

END OF MANAGEMENT TOOL


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GENE	MUTATION	INTERPRETATION
CHEK2	c.1100del (p.Thr367Metfs*15) Heterozygous	High Risk This patient has CHEK2-associated cancer risk.

DETAILS ABOUT: CHEK2 c.1100del (p.Thr367Metfs*15): NM_007194.3
Functional Significance: Deleterious - Abnormal Protein Production and/or Function

The heterozygous germline *CHEK2* mutation c.1100del is predicted to result in the premature truncation of the *CHEK2* protein at amino acid position 381 (p.Thr367Metfs*15).

Clinical Significance: High Risk

This mutation is associated with increased cancer risk and should be regarded as clinically significant.

ADDITIONAL FINDINGS: NO VARIANT(S) OF UNCERTAIN SIGNIFICANCE (VUS) IDENTIFIED

Details About Non-Clinically Significant Variants: All individuals carry DNA changes (i.e., variants), and most variants do not increase an individual's risk of cancer or other diseases. When identified, variants of uncertain significance (VUS) are reported. Likely benign variants (Favor Polymorphisms) and benign variants (Polymorphisms) are not reported and available data indicate that these variants most likely do not cause increased cancer risk. Present evidence does not suggest that non-clinically significant variant findings be used to modify patient medical management beyond what is indicated by the personal and family history and any other clinically significant findings.

Variant Classification: Myriad's myVision™ Variant Classification Program performs ongoing evaluations of variant classifications. In certain cases, healthcare providers may be contacted for more clinical information or to arrange family testing to aid in variant classification. When new evidence about a variant is identified and determined to result in clinical significance and management change, that information will automatically be made available to the healthcare provider through an amended report.

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Name: Voelker, Kevin

DOB: [REDACTED]

Accession #: 05258003-BLD

Report Date: Jan 29, 2025

ADDITIONAL INFORMATION

Genes Analyzed: Sequencing (seq) and large rearrangement analyses were performed for all coding exons in the following genes, unless otherwise indicated:

APC, ATM, AXIN2, BAP1, BARD1, BMPR1A, BRCA1, BRCA2, BRIP1, CDH1, CDK4, CDKN2A, CHEK2, CTNNA1, FH, FLCN, HOXB13 (seq only), MEN1, MET, MLH1, MSH2, MSH3 (excluding repetitive portions of exon 1), MSH6, MUTYH, NTHL1, PALB2, PMS2, PTEN, RAD51C, RAD51D, SDHA, SDHB, SDHC, SDHD, SMAD4, STK11, TP53, TSC1, TSC2, VHL.

Limited promoter regions may also be analyzed for large rearrangements.

Sequencing (seq) and/or large rearrangement (LR) analyses were performed only for the gene portions indicated in parenthesis for the following genes:

EGFR (exons 18-21, seq and LR), EPCAM (exons 8-9, LR only), GREM1 (exon 1 and upstream regulatory regions, LR only), MITF (c.952, seq only), POLE (exonuclease domain, seq only), POLD1 (exonuclease domain, seq only), RET (exons 5, 8, 10, 11, 13-16 seq and LR), TERT (promoter region 71 bases upstream of the translation start, c.-71_-1, seq only).

** Other genes not analyzed with this test may also be associated with cancer.

Indication for Testing: It is our understanding that this individual was identified for testing due to a personal or family history suggestive of a hereditary predisposition for cancer.

Patient Information: Sex assigned at birth is a label given to an individual at birth, typically "male" or "female". In this report, the terms "male", "female", "he", "she", "woman", and "man" refer to sex assigned at birth.

Associated Cancer Risks and Clinical Management: The "MyRisk Management Tool" associated with this report provides a summary of cancer risk and professional society medical management guidelines that may be useful in developing a plan for this patient based on any clinically significant test results and/or reported personal/family history. In some cases, a MyRisk Management Tool cannot be provided, such as when the result has a special interpretation or includes a mutation with unusual characteristics.

Analysis Description: The Technical Specifications summary (myriad.com/technical-specifications) describes the analysis, method, performance, nomenclature, and interpretive criteria of this test. Current testing technologies are unable to definitively determine whether a variant is germline or somatic in origin, which may significantly impact risk estimates and medical management; therefore, these results should be correlated with this patient's personal and family history. The interpretation of this test may also be impacted if the patient has a hematologic malignancy or an allogeneic bone marrow transplant.

CLASSIFICATION DISCLAIMER

THE CLASSIFICATION AND INTERPRETATION OF ALL VARIANTS IDENTIFIED IN THIS ASSAY REFLECTS THE CURRENT STATE OF MYRIAD'S SCIENTIFIC UNDERSTANDING AT THE TIME THIS REPORT WAS ISSUED. VARIANT CLASSIFICATION AND INTERPRETATION MAY CHANGE FOR A VARIETY OF REASONS, INCLUDING BUT NOT LIMITED TO, IMPROVEMENTS TO CLASSIFICATION TECHNIQUES, AVAILABILITY OF ADDITIONAL SCIENTIFIC INFORMATION, AND OBSERVATION OF A VARIANT IN MORE PATIENTS.

Please contact Myriad Medical Services at 1-800-469-7423 X 3850 to discuss any questions regarding this result.

These test results should only be used in conjunction with the patient's clinical history and any previous analysis of appropriate family members. The patient's clinical history and test results should not be disclosed to a third party, unless related to treatment or payment for treatment, without the patient's express written authorization. It is strongly recommended that these results be communicated to the patient in a setting that includes appropriate genetic consultation. This test was developed and its performance characteristics determined by Myriad Genetic Laboratories. It has not been cleared or approved by the U.S. Food and Drug Administration (FDA). The FDA has determined that clearance or approval for laboratory-developed tests is not required.

Genetic testing was completed by CLIA and CAP accredited laboratories in the United States located at: 320 Wakara Way, Salt Lake City, UT 84108 and 322 N 2200 W, Salt Lake City, UT 84116 CLIA IDs: 46D0880690, 46D2275645

The following personnel codes and laboratory director signature may reflect remote review of digital data: 572, 3028


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Integrated BRACAnalysis® with MyRisk™ Hereditary Cancer Test
Clinical & Cancer Family History Information
MyRisk™
 Hereditary Cancer Test

RECEIVING HEALTHCARE PROVIDER	SPECIMEN	PATIENT
Frederick Dold, MD Alliance Cancer Specialists 1311 BRISTOL PIKE STE 100 BENSalem, PA 19020	Specimen Type: Blood Draw Date: Jan 14, 2025 Accession Date: Jan 15, 2025 Report Date: Jan 29, 2025	Legal Name: Voelker, Kevin Date of Birth: [REDACTED] Patient ID: Sex at Birth: M Accession #: 05258003-BLD Requisition #: 11770109

PERSONAL / FAMILY CANCER HISTORY SUMMARY		
FAMILY MEMBER	CANCER / CLINICAL DIAGNOSIS	AGE AT DIAGNOSIS
Patient	Kidney/Renal	63
Family History	None	

The clinical information displayed here was provided by a qualified healthcare provider on the Test Request Form and other documents, and was not verified by Myriad. Female relatives refers to sex assigned at birth, which is a label given to an individual at birth, typically "male" or "female". Family members listed as "other" are not included in a Tyrer-Cuzick breast cancer risk estimate or other personal/family history assessments. For more information see the Specifications for Personal/Family History Analysis at <http://myriad.com/technical-specifications>.

The accuracy and completeness of the information provided in the Clinical and Cancer Family History Information section of the report (e.g. height and weight, age of menarche) may significantly affect the accuracy of breast cancer risk estimates provided based on either Tyrer-Cuzick or RiskScore. The impact of breast surgeries and hormone therapy (except hormone replacement therapy) have not been assessed or validated for Tyrer-Cuzick and RiskScore.

RiskScore is not valid, and may significantly over- or under-estimate breast cancer risk for individuals who do not meet the eligibility criteria in effect when the testing was performed. The current criteria are: 1) sex assigned at birth is female 2) age is 18 to 84 years, 3) no personal history of breast cancer, LCIS, hyperplasia (with or without atypia), or a breast biopsy with unknown results, 4) there is no mutation detected in a breast cancer risk gene (other than a monoallelic CHEK2 mutation in a White/Non-Hispanic or Ashkenazi Jewish individual), 5) the individual's relatives have not been found to have a mutation in a high-penetrance breast cancer risk gene (BRCA1, BRCA2, CDH1, PALB2, PTEN, STK11, TP53, a biallelic mutation in CHEK2, or the specific mutation c.7271T>G (p.Val2424Gly) in ATM) and 6) the sample was submitted with a current Test Request Form and the ordering healthcare provider has not determined that RiskScore is inappropriate for the patient. If this is an amended report for a patient tested in the past, please refer to the MyRisk Technical Specifications at <http://myriad.com/technical-specifications> for the eligibility criteria in effect at the time of the original testing.

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 genetics

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 Clinical Information
 Page 1 of 1



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Integrated BRACAnalysis® with MyRisk™ Hereditary Cancer Test

MyRisk Management Tool

MyRisk™
 Hereditary Cancer Test

RECEIVING HEALTHCARE PROVIDER

 Frederick Dold, MD
 Alliance Cancer Specialists
 1311 BRISTOL PIKE STE 100
 BENSalem, PA 19020

SPECIMEN

 Specimen Type: Blood
 Draw Date: Jan 14, 2025
 Accession Date: Jan 15, 2025
 Report Date: Jan 29, 2025

PATIENT

 Legal Name: Vosker, Kevin
 Date of Birth: [REDACTED]
 Patient ID: [REDACTED]
 Sex at Birth: M
 Accession #: 05258003-BLD
 Requisition #: 11770109

GENETIC RESULT: POSITIVE - CLINICALLY SIGNIFICANT MUTATION IDENTIFIED

CLINICAL HISTORY ANALYSIS: NO ADDITIONAL MANAGEMENT GUIDELINES IDENTIFIED
BASED ON THE CLINICAL HISTORY PROVIDED

Other clinical factors may influence individualized management. This analysis may be incomplete if details about cancer diagnoses, ages, family relationships or other factors were omitted or ambiguous. If this patient also has a clinically significant mutation, the recommendations based on the clinical history analysis should be considered in light of the possibility that this mutation explains all or some of the cancer history in the family.

GENE

MUTATION

THIS GENETIC TEST RESULT IS ASSOCIATED WITH THE FOLLOWING CANCER RISKS:

CHEK2

c.1100del (p.Thr367Metfs*15)
Heterozygous

ELEVATED RISK: Male Breast, Colorectal

Please see the Genetic Test Result for more details on any variant(s) detected in this patient, including variant classification information.

The terms "male", "female", "he", "she", "women", and "men" refer to sex assigned at birth.

ADDITIONAL FINDINGS: NO VARIANT(S) OF UNCERTAIN SIGNIFICANCE (VUS) IDENTIFIED

CLINICAL OVERVIEW OF GENETIC FINDINGS

CHEK2-associated cancer risk

- This patient has been found to have a mutation in the *CHEK2* gene. Most women with *CHEK2* mutations have a risk for breast cancer that is significantly increased over the 12.5% lifetime risk for women in the general population of the United States. Men with *CHEK2* mutations also have an increased risk for breast cancer.
- Estimates of cancer risk for men and women with *CHEK2* mutations vary widely and are strongly influenced by family history. In cases where there is no family history of one of these cancers, the risk for a patient with a *CHEK2* mutation may be lower than in cases where that cancer has been diagnosed in one or more close relatives. Therefore, the family history of a patient should be considered when deciding on the most appropriate strategies to manage cancer risk, with more aggressive strategies targeted to patients with significant family histories of related cancers.
- Individuals with *CHEK2* mutations may have an elevated risk for colorectal cancer, and the National Comprehensive Cancer Network (NCCN) has provided screening recommendations to address this possible risk.
- Some studies have described a possible increased risk for a wide range of cancers in patients with *CHEK2* mutations, including prostate, gastric, thyroid, renal, hematological malignancies, testicular germ cell tumors, and other malignancies. However, these studies are not conclusive and there are currently no medical management guidelines to address these possible risks.

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Name: Voelker, Kevin

DOB: [REDACTED]

Accession #: 05258003-BLD

Report Date: Jan 29, 2025

- Although there are increased risks for cancer in men and women with mutations in *CHEK2*, there are interventions that may reduce these risks. Guidelines from the National Comprehensive Cancer Network (NCCN) that may apply are listed below. Since information about the cancer risks associated with *CHEK2* mutations is relatively new, and there is still some uncertainty about the best ways to reduce these risks, it may be appropriate to interpret these results in consultation with cancer genetics experts in this emerging area of knowledge.

WHAT ARE THE PATIENT'S CANCER RISKS?

These risk tables show the clinically significant cancer risks identified as part of this patient's testing. Testing for some patients does not include some of the analyses listed:

- GENETIC RESULT: Mutations detected in any of the hereditary cancer genes included on the MyRisk panel.
- BREAST CANCER RISKS: RiskScore estimate of remaining lifetime breast cancer risk if 20% or greater
- CLINICAL HISTORY ANALYSIS for breast cancer risk: Tyrer-Cuzick model estimate of remaining lifetime breast cancer risk of 20% or greater
- CLINICAL HISTORY ANALYSIS for breast, colorectal, pancreatic, prostate and melanoma cancer: Analysis of the patient's personal and family history.

The risks for each of these results are provided separately. If the risk for any individual cancer is affected by more than one of these results, the risk associated with each finding is listed in a separate table. At this time, there is not enough information to estimate risks for cancers affected by more than one gene mutation, or risks based on both gene mutations and personal/family history.

Risks Due to *CHEK2*-associated cancer risk

CANCER TYPE	CANCER RISK	RISK FOR GENERAL POPULATION	RELATED TO
MALE BREAST			
To age 80	0.4%-1%	0.1%	<i>CHEK2</i>
COLORECTAL			
To age 80	Possibly elevated risk	2.8%	<i>CHEK2</i>

WHAT MANAGEMENT FOR CANCER RISKS SHOULD BE CONSIDERED?

This overview of clinical management guidelines is based on the patient's genetic test results and the Clinical History Analysis. Medical management guidelines are summarized from established medical societies, primarily the National Comprehensive Cancer Network (NCCN). If there are overlapping management guidelines for any individual cancer due to more than one of these results, the guidelines associated with each finding are listed in separate tables, even if they are the same. At this time, there are no medical society guidelines for how to adjust management when there are multiple sources of risk, such as from more than one gene mutation, or a mutation and a personal/family history of cancer. In these cases, it may be appropriate to use the most aggressive of the management options provided.

The overview provided below should not be used as the sole source of information to determine medical management. The references cited should always be consulted for more details and updates to the recommendations.

No information is provided related to treatment of a previous or existing cancer or polyps. The recommendation summaries below may require modification due to the patient's personal medical history, past surgeries and other treatments. Patients with a past history of cancer, benign tumors, or pre-cancerous findings may be candidates for long term surveillance and risk-reduction strategies beyond what is necessary for the treatment of their initial diagnosis. Any discussion of medical management options is for general information purposes only and does not constitute a recommendation. While genetic testing and medical society recommendations provide important and useful information, medical management decisions should be made in consultation between each patient and his or her healthcare provider.

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Management Options for CHEK2-associated cancer risk

PROCEDURE	AGE TO BEGIN	FREQUENCY	RELATED TO
MALE BREAST			

Currently there are no specific medical management guidelines for male breast cancer risk in mutation carriers. However, the increase in risk warrants consideration of options for male breast cancer screening, such as patient breast awareness education and clinical breast examinations.^{1,2}

Individualized

NA

CHEK2

COLORECTALColonoscopy³

40 years, or 10 years younger than the age of diagnosis for any first-degree relative with colorectal cancer

Every 5 years

CHEK2

FOR PATIENTS WITH A CANCER DIAGNOSIS

For patients with a gene mutation and a diagnosis of cancer, targeted therapies may be available as a treatment option for certain tumor types (e.g., PARP-inhibitors).⁴

NA

NA

CHEK2

1. Bevers TB, et al. NCCN Clinical Practice Guidelines in Oncology®: Breast Cancer Screening and Diagnosis. V 1.2022. Jun 2. Available at <https://www.nccn.org>.

2. Daly M et al. NCCN Clinical Practice Guidelines in Oncology®: Genetic/Familial High-Risk Assessment: Breast, Ovarian and Pancreatic. V 3.2023. Feb 13. Available at <https://www.nccn.org>.

3. Gupta S, et al. NCCN Clinical Practice Guidelines in Oncology® Genetic/Familial High-Risk Assessment: Colorectal. V 1.2023. May 30. Available at <https://www.nccn.org>.

4. Schaeffer E, et al. NCCN Clinical Practice Guidelines in Oncology®: Prostate Cancer. V 1.2023. Sep 16. Available at <https://www.nccn.org>.

Notes for Personalized Management:

INFORMATION ON HOW CANCER RISKS AND MANAGEMENT ARE DETERMINED

The MyRisk Management Tool provides cancer risk levels based on analysis of genetic test results (see MyRisk Genetic Result) and a summary of medical society management recommendations based on both the genetic test results and a limited analysis of the patient's clinical history related to the risk for breast, colorectal, prostate, melanoma and pancreatic cancers. Here are some important points to understand as you interpret this test report and decide on the best plan for management:

- Comprehensive patient management. The management recommendations presented in this report are a summary of management options recommended by the National Comprehensive Cancer Network (NCCN) and other established medical societies and are general in nature. The patient's actual management should be modified based on personal medical history, surgeries and other treatments. A comprehensive risk assessment and management plan may take into account this report and other aspects of the patient's personal/family medical history (e.g., all known clinical diagnoses), as well as lifestyle, environmental and other factors.

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- Risk estimates based on provider-supplied information. Some of the risk estimates and management recommendation summaries provided in this report are based on our interpretation of information supplied by the ordering health care provider on the test request form (see Specifications for Personal/Family History analysis at myriad.com/technical-specifications). The patient's actual risks and appropriate management may be significantly different if details provided for cancer diagnoses, ages, family relationships or other factors were incorrect, omitted, ambiguous or have since changed. Please review the clinical history listed on the Clinical & Family History Information page of this report to make sure that the information used was provided and interpreted correctly.
- Variability in Tyer-Cuzick risk estimates. Tyer-Cuzick estimates of breast cancer risk can vary significantly based on the way in which the model is used, and the estimate provided here may be higher or lower than what would be calculated by other users. For complete details of how Myriad calculates Tyer-Cuzick risk estimates, including how Myriad handles information provided in a format not compatible with the model, please see the Specifications for Personal/Family History analysis at myriad.com/technical-specifications. These Specifications also include information for recalculating the Tyer-Cuzick breast cancer risk estimate if desired.
- What is meant by "High Risk" and "Elevated Risk"? In the Genetic Test Result Summary, a gene-associated cancer risk is described as "High Risk" for a cancer type if all of the following conditions are met: the absolute risk of cancer is approximately 5% or higher, the increase in risk over the general population is approximately 2 to 3-fold or higher, and there is significant data from multiple studies supporting the cancer risk estimate. A gene is described as "Elevated Risk" for a cancer type if there is sufficient data to support an increase in cancer risk over the general population risk, but not all criteria for "High Risk" are met.

INFORMATION FOR FAMILY MEMBERS

Family members should talk to their healthcare providers about hereditary cancer testing to help define their own risk and assist in the interpretation of this patient's genetic test result.

- This patient's relatives are at risk for carrying the same mutation(s) and associated cancer risks as this patient. Cancer risks for individuals who have this/these mutation(s) are provided below.
- Family members should talk to a healthcare provider about genetic testing. Close relatives such as parents, children, and siblings have the highest chance of having the same mutation(s) as this patient. Other more distant relatives such as cousins, parents' siblings, and grandparents also have a chance for carrying the same mutation(s). Testing of at-risk relatives can identify those family members with the same mutation(s) who may benefit from surveillance and early intervention. More resources for family testing are available at MySupport360.com.

Additional Information for CHEK2-associated cancer risk

- In rare instances, an individual may inherit mutations in both copies of the *CHEK2* gene, leading to significantly higher breast cancer risks than those in women with a single *CHEK2* mutation. The children of this patient are at risk of inheriting two *CHEK2* mutations only if the other parent is also a carrier of a *CHEK2* mutation. Screening the other biological parent of any children for *CHEK2* mutations may be appropriate. Alternatively, this patient's children may consider genetic testing for any mutations in the entire *CHEK2* gene.

CANCER RISK FOR CHEK2 CLINICALLY SIGNIFICANT MUTATION

CANCER TYPE	CANCER RISK	RISK FOR GENERAL POPULATION
FEMALES		
FEMALE BREAST		
To age 80	20%-31%	10.7%
Second primary within 10 years of first breast cancer diagnosis	7%-29%	3.5%
MALES		
MALE BREAST		
To age 80	0.4%-1%	0.1%

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Accession #: 05258003-BLD

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CANCER RISK FOR CHEK2 CLINICALLY SIGNIFICANT MUTATION

CANCER TYPE	CANCER RISK	RISK FOR GENERAL POPULATION
		FEMALES AND MALES
COLORECTAL	To age 80	Possibly elevated risk 2.8%

Please contact Myriad Medical Services at 1-800-469-7423 X 3850 to discuss any questions regarding this result.

END OF MANAGEMENT TOOL



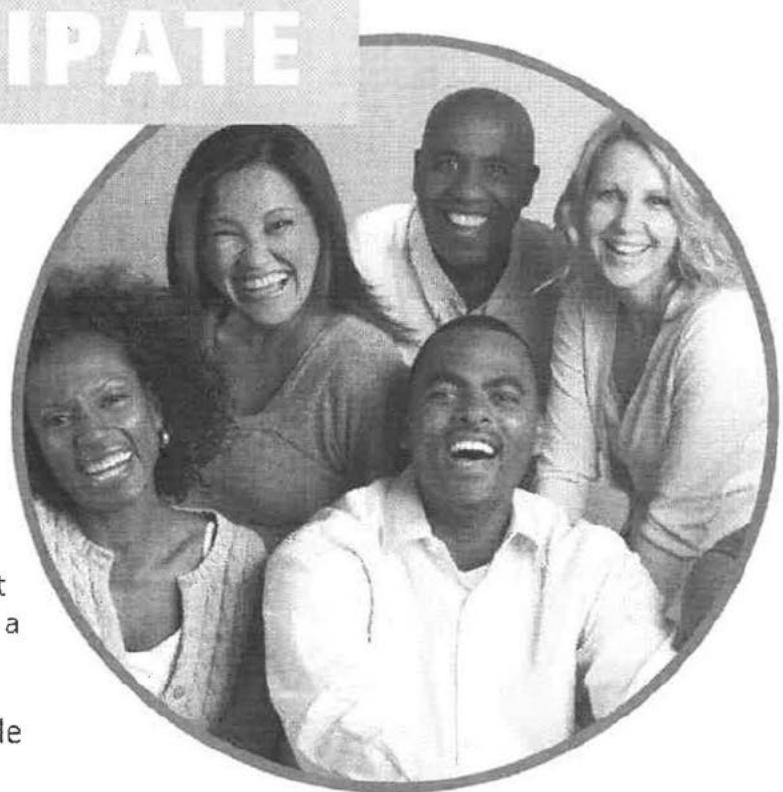
WHY PARTICIPATE IN ICARE?

Be a part of new discoveries.

Studies that used information from
ICARE participants have...

found that removing the ovaries may not
lower breast cancer risk for women with a
BRCA mutation.¹

improved cancer risk estimates for people
with **PALB2** mutations.²



Get care updates personalized to you.

as new guidelines and other information come out – for example:

ICARE participants with mutations in **PALB2**, **CHEK2**, and **ATM** were given updates that might affect their care because new National Comprehensive Cancer Network (NCCN) Genetics Guidelines were released in September 2022.

Find out about other studies.

Examples of studies include:

A study providing free resources to help with
managing cancer risks and family communication
of test results.

A study doing free genomic studies on breast
cancers in people with **BRCA1**, **BRCA2**, **PALB2**,
ATM, and **CHEK2** mutations to learn more
about how these tumors develop and how
we might best treat them.

Enroll online by visiting
<https://redcap.link/ICAREconsent>
or scan the below QR code:



05258003-BLD



Prospective Registry Of MultiPlex Testing

Opportunity to Enroll in Hereditary Cancer Research

Genetic testing can help individuals and families by giving them a clearer idea of their cancer risks. Genetic tests (called multi-gene or multiplex panels) look for changes in several different genes, all in a single test. While all of the genes on these panels have been tied to an increased risk of cancer, we understand the risks associated with some of the genes better than we understand others. One way to help improve our understanding is to enroll people with pathogenic mutations or variants of unknown significance in registries. Registries typically follow people over many years to learn more about these alterations and how they impact their health.

How can I find a research registry?

There are several hereditary cancer research registries that are studying individuals who have had multiplex panel testing. One registry that is open to individuals nationwide is PROMPT (or **Prospective Registry Of MultiPlex Testing**). PROMPT is an online registry for patients and families who have had multiplex testing and have been found to have a genetic variation which may be linked to an increased risk of cancer. PROMPT is a joint effort involving several academic medical centers and commercial laboratories, working together to learn more about the genes that are studied on multiplex panels. PROMPT will allow researchers to better understand the cancer risks associated with changes in these genes and thus provide a better understanding of the best way to take care of individuals who have such changes.

What is involved in participation?

Participation in the study simply involves completing online surveys. Additionally, the PROMPT team may reach out to you to talk about ways that you can get more involved with the research effort. Your participation will help researchers learn more and improve the ability of this genetic testing to help people.

How do I enroll?

You can learn more about or register for PROMPT by going to www.promptstudy.info or by scanning the QR code below.

Thank you again for considering taking part in PROMPT!



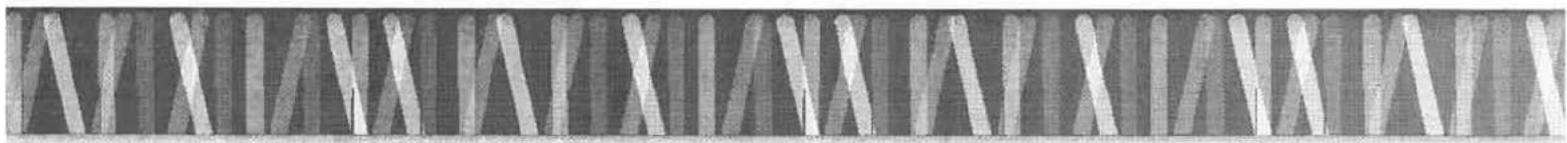
If you would like to read more about multiplex panels, including details about specific genes, please visit our informational website at www.promptstudy.info.



 Positive result

Understanding a positive result

A guide to understanding risk and taking action



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05258003-BLD



Understanding your Myriad MyRisk™ hereditary cancer test result

Your Myriad Genetics MyRisk Hereditary Cancer test has three main sections which are summarized in the banner on the first page. Throughout the report, these sections can be identified by the title on the top left of each page of the report.

- ① Genetic result
- ② Clinical & cancer family history information
- ③ Management tool

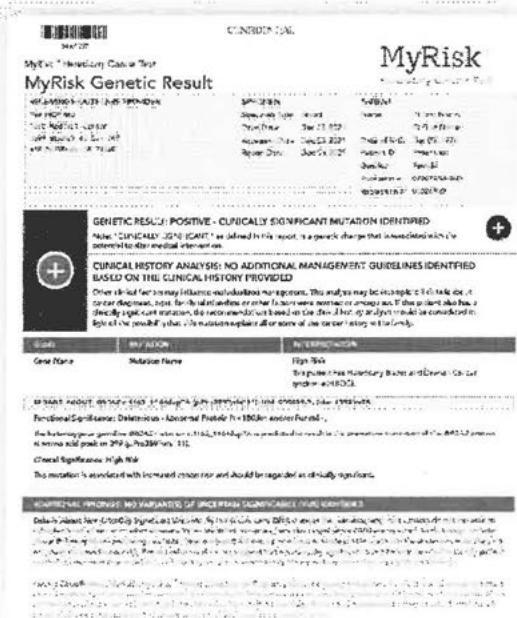
① Genetic result

The MyRisk test looks at multiple genes associated with hereditary cancer risk. When a gene has a clinically significant mutation, or harmful change, there is a higher chance for certain cancers to develop. A list of the genes evaluated on your test can be found in this section of your report. The gene table on our website includes information about each gene and the cancers with which it is associated.

Your genetic result was **POSITIVE**.

This means that a clinically significant mutation, or harmful genetic change, was found in one or more of the genes analyzed as part of your testing. Since genes are passed down in families, your close relatives, such as your children, brothers and sisters, parents, aunts and uncles, and cousins, are at risk to have the same genetic change that was identified in you. It is important to share your results with your relatives so they can discuss genetic testing with their own healthcare providers.

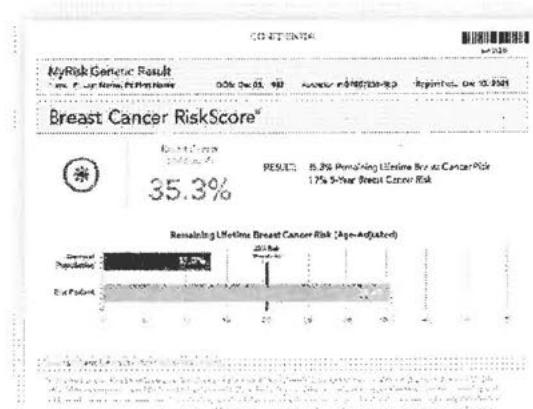
If a variant of uncertain clinical significance (VUS) was identified, it will also be listed in the genetic result section. A VUS is a genetic change that may or may not be contributing to your cancer risk. A VUS is not considered to be clinically actionable, so medical care decisions should not be made based on a VUS. We are committed to identifying information so that we can better understand these genetic changes. If new information is available about your specific VUS, that information will be shared with your healthcare provider.



Positive results with SINGLE SITE testing: If a member of your family has tested positive for a clinically significant mutation, your provider may have ordered testing for only that specific genetic change. This is known as single site testing. Your positive result means that you DO carry the same harmful genetic change that was found in your family member and you should discuss any changes to your medical management that should be considered with your healthcare provider. Since single site testing does not look for other genetic changes or assess additional risk from family history, this is not a comprehensive risk assessment. Information in the management tool is specific ONLY to the clinically significant mutation listed on your report.

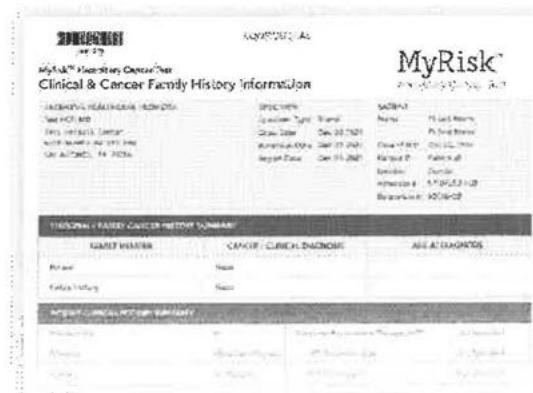
Breast cancer RiskScore™

You may or may not see a breast cancer RiskScore and/or a Tyrer-Cuzick breast cancer risk assessment in this section of the report. These results are calculated for women who meet certain criteria and have never been diagnosed with breast cancer themselves.



2 Clinical & cancer family history information

The Clinical & Cancer Family History Information section reviews the medical information that your healthcare provider gave us about you and your family. Certain types of cancer in the family or cancers diagnosed at early ages can indicate that someone may have an elevated risk, even if no clinically significant mutations are found.



③ Management tool

In this section of the result, there will be a table for each gene in which a clinically significant mutation was identified. This table outlines associated cancers and the risk to develop these cancers. In another table, a summary of medical management options from expert medical groups for these cancers and/or a list of other health problems associated with the mutation are included. The medical management options may include changes to screening frequency or recommendations for a specific type of screening, discussions about preventive surgery, consideration of preventive medication, and/or lifestyle changes.

In addition to the genetic result, the presence of certain cancers in the family or certain medical findings in your own health history can also influence your cancer risk. There may be additional recommendations listed in this section due to these personal or family history health factors. If there are recommendations for changes to your breast cancer screening based on your RiskScore™ and/or a Tyrer-Cuzick breast cancer risk assessment, they will be included in this section. Personal and family histories can change over time, so it is important to keep your healthcare providers up to date regarding any changes.



Resources

Your healthcare provider is always your primary resource. You can request a consultation with a genetic counselor at Myriad by going to my.myriad.com/consults. During your consultation, the genetic counselor can help you understand your report and the implications of your results.

To view the full list of genes available on the MyRisk™ panel, please visit:
www.myriadmyrisk.com/gene-table/

Next steps



Schedule any follow-up appointments and/or obtain referrals to appropriate specialists



Speak with your relatives about your results and encourage them to see their healthcare provider about cancer prevention and genetic testing



Consider speaking with a **clinical genetic counselor** or other genetics expert in your community about your test result and family history



Myriad Genetics, Inc.
320 Wakara Way
Salt Lake City, UT
84108

myriad.com

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Aids and Services

Myriad provides free aids and services to people with disabilities to communicate effectively with us, such as TTY/TDD calls or written information in suitable formats. Myriad will also provide free language services to people whose primary language is not English through qualified interpreters.

If you need these services, contact:

Don Martin
Chief Compliance Officer
320 Wakara Way
Salt Lake City, UT 84108

Telephone: (801) 584-3600
Fax: (801) 584-3640
Email: compliance@myriad.com

Grievances

- If you believe that Myriad has failed to provide these services or discriminated in another way on the basis of race, color, national origin, age, disability, or sex. You can file a grievance by mail, telephone, fax, or email. If you need help filing a grievance, Mr. Martin is available to help you (see contact information above).

Grievance Procedure

- Any person who believes someone has been subjected to discrimination by Myriad on the basis of race, color, national origin, sex, age or disability may file a grievance with Myriad. It is against the law for Myriad to retaliate against anyone who opposes discrimination, files a grievance, or participates in the investigation of a grievance.
- Grievances must be submitted within 60 days of the date the person filing the grievance becomes aware of the alleged discriminatory action.
- The complaint must be in writing, containing the name and address of the person filing it. The complaint must state the problem or action alleged to be discriminatory and the remedy or relief sought.
- Myriad will conduct an investigation of the complaint. This investigation may be informal, but it will be thorough, affording all interested persons an opportunity to submit evidence relevant to the complaint. Myriad will maintain the files and records relating to such grievances. To the extent possible, and in accordance with applicable law, Myriad will take appropriate steps to preserve the confidentiality of files and records relating to grievances and will share them only with those who have a need to know.
- Myriad will issue a written decision on the grievance, based on a preponderance of the evidence, no later than 30 days after its filing, including a notice to the complainant of their right to pursue further administrative or legal remedies.
- The person filing the grievance may appeal Myriad's decision in writing to the Chief Executive Officer (CEO) of Myriad within 15 days of receiving Myriad's initial decision. The CEO will issue a written decision in response to the appeal no later than 30 days after its filing.
- Individuals seeking access to Section 1557 and its implementing regulations may be facilitated by contacting Mr. Martin (see contact information above).
- The availability and use of this grievance procedure does not prevent a person from pursuing other legal or administrative remedies, including filing a complaint of discrimination on the basis of race, color, national origin, sex, age or disability in court or with the U.S. Department of Health and Human Services, Office for Civil Rights. A person can file a complaint of discrimination electronically through the Office for Civil Rights Complaint Portal, which is available at: <https://ocrportal.hhs.gov/ocr/portal/lobby.jsf>, or by mail or phone at:

U.S. Department of Health and Human Services
200 Independence Avenue, SW
Room 509F, HHH Building
Washington, D.C. 20201

- Complaints must be filed within 180 days of the date of the alleged discrimination. Myriad will make appropriate arrangements to ensure that individuals with disabilities and individuals with limited English proficiency are provided auxiliary aids and services or language assistance services, respectively, if needed to participate in this grievance process. Mr. Martin will be responsible for such arrangements.

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Español (Spanish)

Myriad Genetics, Inc. cumple con las leyes federales de derechos civiles aplicables y no discrimina por motivos de raza, color, nacionalidad, edad, discapacidad o sexo.

ATENCIÓN: si habla español, tiene a su disposición servicios gratuitos de asistencia lingüística. Llame al 1-801-584-3600.

繁體中文 (Chinese)

Myriad Genetics, Inc. 遵守適用的聯邦民權法律規定，不因種族、膚色、民族血統、年齡、殘障或性別而歧視任何人。

注意：如果您使用繁體中文，您可以免費獲得語言援助服務。請致電1-801-584-3600。

한국어 (Korean)

Myriad Genetics, Inc. 은(는) 관련 연방 공민권법을 준수하며 인종, 피부색, 출신 국가, 연령, 장애 또는 성별을 이유로 차별하지 않습니다.
주의: 한국어를 사용하시는 경우, 언어 지원 서비스를 무료로 이용하실 수 있습니다. 1-801-584-3600. 번으로 전화해 주십시오.

Tagalog (Tagalog - Filipino)

Sumusunod ang Myriad Genetics, Inc. sa mga naaangkop na Federal na batas sa karapatang sibil at hindi nandiskrimina batay sa lahi, kulay, bansang pinagmulan, edad, kapansanan o kaserian.

PAUNAWA: Kung nagsasalita ka ng Tagalog, maaari kang gumamit ng mga serbisyo ng tulong sa wika nang walang bayad. Tumawag sa 1-801-584-3600.

